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Applicant Initiated Interview Request Form

Application No.: 10/733,847 First Named Applicant: Peter A. Carr
Examiner: Lu, Frank Wei Min Art Unit: 1634 Status of Application: Final rejection

Tentative Participants:
(1) Examiner Lu (2) Norma E. Henderson, Attorney for Applicants
(3) (4)

Proposed Date of Interview: Friday, May 14 **Proposed Time:** 10:30 AM **(AM/PM)**

Type of Interview Requested:
(1) [✓] Telephonic (2) [ ] Personal (3) [ ] Video Conference

Exhibit To Be Shown or Demonstrated: [ ] YES [✓] NO
If yes, provide brief description:

Issues To Be Discussed

Issues (Rej., Obj., etc)	Claims/ Fig. #s	Prior Art	Discussed	Agreed	Not Agreed
(1) Obj. (Item #2)	13		[ ]	[ ]	[ ]
(2) Rej. 112, para 1	11		[ ]	[ ]	[ ]
(3) Rej. 112, para 2	11, 12, 21		[ ]	[ ]	[ ]
(4) Rej. 112, para 2	15, 21, 26, 29		[ ]	[ ]	[ ]

[ ] Continuation Sheet Attached
[✓] Proposed Amendment or Arguments Attached
Brief Description of Arguments to be Presented:

Proposed amendments are made to adopt the Examiner's suggestions for Office Action items # 2, 4, 7, 9, and 11-13, explanation and minor amendment are made re Office Action item #8, and item #10 is traversed.

An interview was conducted on the above-identified application on _____.
NOTE: This form should be completed by applicant and submitted to the examiner in advance of the interview (see MPEP § 713.01).
This application will not be delayed from issue because of applicant's failure to submit a written record of this interview. Therefore, applicant is advised to file a statement of the substance of this interview (37 CFR 1.133(b)) as soon as possible.

Applicant/Applicant's Representative Signature — Examiner/SPE Signature

Norma E. Henderson
Typed/Printed Name of Applicant or Representative

39219
Registration Number, if applicable

Proposed claim amendments for 5/14/2010 Applicant-Initiated Interview

Listing of Claims:

1-10. (cancelled)

11. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being synthesized to have a user-specified sequence and length by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;

b) distinguishing between error-free and error-containing nucleic acid molecules within said plurality or pool; and

c) selectively amplifying only the error-free nucleic acid molecules from said plurality or pool, thereby decreasing the ~~percentage~~ relative amount of error-containing nucleic acid molecules within said plurality or pool.

12. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being synthesized to have a user-specified sequence and length by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;

b) distinguishing between error-free and error-containing nucleic acid molecules within said plurality or pool; and

c) correcting errors in said plurality or pool by using the error-free nucleic acid molecules in said plurality or pool as a template for repair of said error-containing nucleic acid molecules.

13. (currently amended) A method for removing or controlling errors in nucleic acid molecules comprising arbitrary user-specified sequence composition and length, the method comprising:

a) providing a plurality or pool of nucleic acid molecules, the nucleic acid molecules being synthesized to have a user-specified sequence and length by the steps of:

providing a first immobilized nucleic acid comprising a first 5' region and a first 3' region;

providing at least a second immobilized nucleic acid comprising a second 5' region and a second 3' region, wherein said second 3' region and said first 5' region comprise identical nucleic acid sequences;

contacting said first immobilized nucleic acid with an oligonucleotide under conditions promoting hybridization of said oligonucleotide to said first 3' region and extension of said hybridized oligonucleotide to produce a first extension product comprising a first extension product 3' region that is complementary to said first 5' region; and

contacting said second immobilized nucleic acid with said first extension product under conditions promoting hybridization of said first extension product 3' region to said second 3' region and extension of said hybridized extension product 3' region to produce a second extension product comprising a second extension product 3' region that is complementary to said second 5' region, wherein said second extension product comprises said complementary first and second 3' and 5' regions, and said nucleic acid molecule comprises said second extension product;

b) identifying error-containing nucleic acid molecules ~~ones~~ of said nucleic acid molecules;

c) removing the error-containing portions of said error-containing nucleic acid molecules to produce error-free nucleic acid sequences; and

d) ~~recombining~~ combining said error-free nucleic acid sequences to yield error-free nucleic acid molecules.

14. (previously amended) The method of claim 11, the step of selectively amplifying further comprising the step of combining at least one error-containing nucleic acid

molecule from said plurality or pool with at least one component that prevents amplification of the error-containing nucleic acid molecule.

15. (currently amended) The method of claim 14, wherein the errors in the error-containing nucleic acid molecule are mismatches and the component is a mismatch binding protein.

16. (previously presented) The method of claim 14, wherein the component is cross-linked to the error-containing nucleic acid molecule.

17. (cancelled)

18. (cancelled)

19. (previously presented) The method of claim 14, wherein the component comprises more than one molecule.

20. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of targeting errors via methylation and selective demethylation.

21. (currently amended) The method of claim 12, wherein the errors in the error-containing nucleic acid molecules are mismatches, the step of correcting errors comprising the steps of:

mismatch recognition on said error-containing nucleic acid molecules to identify specific base errors in said error-containing nucleic acid molecules;

cleavage of said specific base errors; and

replacement of said cleaved base errors with the correct bases according to the template.

22. (previoustly amended) The method of claim 21, wherein the steps of mismatch recognition and cleavage are performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

23. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by disassociation and reassociation of single-stranded nucleic acid molecules.

24. (withdrawn) The method of claim 12, the step of correcting errors comprising the step of generating at least one repair template by strand invasion.

25. (withdrawn) The method of claim 12, wherein no entire nucleic acid molecules in the plurality or pool need be error-free.

26. (currently amended) The method of claim 13, wherein the errors in the error-containing nucleic acid molecules are mismatches, the step of removing errors comprising the steps of:

mismatch recognition on said error-containing nucleic acid molecules to identify specific base sequence errors in said error-containing nucleic acid molecules; and

cleavage of said specific base sequence errors.

27. (previously amended) The method of claim 26, wherein the steps of mismatch recognition and cleavage are performed by a resolvase, a single-stranded nuclease, or a combination of a mismatch binding protein and a nuclease.

28. (withdrawn) The method of claim 26, wherein the step of mismatch recognition and cleavage is performed by a single molecule.

29. (currently amended) The method of claim 13, wherein the errors in the error-containing nucleic acid molecules are mismatches and the step of removing errors is performed by a mismatch binding protein to identify specific base sequence errors in said

error-containing nucleic acid molecules and a nuclease to cleave said specific base sequence errors.

30. (previously presented) The method of claim 13, wherein no nucleic acid molecules in the plurality or pool need be error-free.

Remarks re Rejections in 11/19/2009 Office Action and Proposed Claim Amendments

Office Action paragraph / Response

2. / Claim 13 amended to adopt the Examiner's suggested change.

4. / Claim 11 amended to return to the original claim language, deleting "percentage" and replacing it with "relative amount", as suggested by the Examiner.

7. / Claim 12 amended to adopt the Examiner's suggested claim language.

8. / Step d) of claim 13 recites the combining of the error-free nucleic acid sequences of step c) into nucleic acid molecules, and thus it is not unnecessary. This is clarified by amending step d) to recite "combining" instead of "recombining".

9. / Claim 15 amended to adopt the Examiner's suggestion and recite that the errors are mismatches.

10. / Traversed. Claim 12 does contain the word "template", in step c) ["c) correcting errors in said plurality or pool by using error-free nucleic acid molecules in said plurality or pool as a template for repair of said error-containing nucleic acid molecules"].

11. / Claim 21 amended similarly to claim 15, adopting the Examiner's suggestion and reciting that the errors are mismatches.

12. / Claim 26 amended similarly to claim 15, adopting the Examiner's suggestion and reciting that the errors are mismatches.

13. / Claim 29 amended similarly to claim 15, adopting the Examiner's suggestion and reciting that the errors are mismatches.